

### **Amendments to the Specification:**

The paragraph, beginning at page 302, line 2, has been amended as follows:

--Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)).  
~~The NCBI-BLAST2 sequence comparison program may be downloaded from~~  
~~<http://www.ncbi.nlm.nih.gov>~~. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

The paragraph, beginning at page 304, line 18, has been amended as follows:

--Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)).  
~~The NCBI-BLAST2 sequence comparison program may be downloaded from~~  
~~<http://www.ncbi.nlm.nih.gov>~~. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

The paragraph, beginning at page 362, line 5, has been amended as follows:

--It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, ~~Sephadex~~SEPHADEX<sup>TM</sup> G-75; ~~protein A~~  
~~Sepharose~~ PROTEIN A-SEPHAROSE<sup>TM</sup> columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example

in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.--

The paragraph, beginning at page 371, line 31, has been amended as follows:

--The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, ~~protein A-Sepharose~~ PROTEIN A-SEPHAROSE™, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.--

The paragraph, beginning at page 378, line 20, has been amended as follows:

--The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g., LIFESEQ™ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).--

The paragraph, beginning at page 386, line 13, has been amended as follows:

--DNA56862-1343 was identified by applying the proprietary signal sequence finding algorithm described in Example 3 above. Use of the above described signal sequence algorithm allowed identification of an EST cluster sequence from the Incyte database, designated Incyte cluster sequence no. 25507. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer

program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program "phrap" (Phil Green, University of Washington). The consensus sequence obtained therefrom is herein designated as DNA55714.--

The paragraph, beginning at page 390, line 15, has been amended as follows:

--A cDNA sequence isolated in the amylase screen described in Example 2 above is herein designated DNA41784. The DNA41784 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and proprietary EST DNA databases (~~LIFESEQ~~<sup>TM</sup> LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA; and Genentech, South San Francisco, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA45499.--

The paragraph, beginning at page 391, line 15, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 150918. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq~~<sup>®</sup> LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the

program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA55720.--

The paragraph, beginning at page 396, line 4, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 7494. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq~~® LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56056.--

The paragraph, beginning at page 398, line 1, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 115204. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq~~® LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56522.--

The paragraph, beginning at page 400, line 12, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 56523. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56103.--

The paragraph, beginning at page 403, line 8, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster no. 122605. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56060.--

The paragraph, beginning at page 407, line 13, has been amended as follows:

--A cDNA sequence isolated in the amylase screen described in Example 2 above is herein designated DNA37721. The DNA37721 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank)

and proprietary EST DNA databases (~~LIFESEQ™~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA; Genentech, South San Francisco, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated “DNA48616”. Based on the DNA48616 sequence, oligonucleotide probes were generated and used to screen a human aortic endothelial cell library prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.--

The paragraph, beginning at page 408, line 14, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 69537. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56034.--

The paragraph, beginning at page 409, line 35, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 56853. This EST cluster sequence was then compared to a variety of expressed

sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56021.--

The paragraph, beginning at page 410, line 28, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 44725. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56023.--

The paragraph, beginning at page 430, line 34, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 40671. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)).

Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56749.--

The paragraph, beginning at page 431, line 25, has been amended as follows:

--Use of the signal sequence algorithm described in Example 3 above allowed identification of an EST cluster sequence from the Incyte database, designated Incyte EST cluster sequence no. 139524. This EST cluster sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~Lifeseq®~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into a consensus DNA sequence with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA56115.--

The paragraph, beginning at page 434, line 35, has been amended as follows:

--A cDNA sequence isolated in the amylase screen described in Example 2 above is herein designated DNA43203. The DNA43203 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and proprietary EST DNA databases (~~LIFESEQ™~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA; Genentech, South San Francisco, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program “phrap” (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is designated herein as “DNA48360”.--



The paragraph, beginning at page 467, line 3, has been amended as follows:

--A cDNA sequence isolated in the amylase screen described in Example 2 above is herein designated DNA47580. The DNA47580 sequence was then compared to a variety of expressed sequence tag (EST) databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (~~LIFESEQ™~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated "DNA57246".--

The paragraph, beginning at page 467, line 12, has been amended as follows:

--In light of the sequence homology between the DNA57246 sequence and EST no. 1793996 from the ~~LIFESEQ™~~ LIFESEQ® database, the clone containing the EST no. 1793996, which originates from a library constructed from prostate tumor tissue, was purchased and the cDNA insert was obtained and sequenced. The sequence of this cDNA insert is shown in Figure 223 (SEQ ID NO:382) and is herein designated as DNA76541-1675.--

The paragraph, beginning at page 472, line 2, has been amended as follows:

--EST databases, which included public EST databases (e.g., GenBank), and a proprietary EST database (~~LIFESEQ™~~ LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA), were searched for sequences having homologies to human UCP3. The search was performed using the computer program BLAST or BLAST2 [Altschul et al., Methods in Enzymology, 266:460-480 (1996)] as a comparison of the UCP3 protein sequences to a 6 frame translation of the EST sequences. Those comparisons resulting in a BLAST score of 70 (or in some cases, 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program AssemblIGN and MacVector (Oxford Molecular Group, Inc.).--

The paragraph, beginning at page 486, line 26, has been amended as follows:

--In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over ~~Lympholyte-M~~ LYMPHOLYTE®-M (cell separation medium) (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to  $1 \times 10^7$  cells/ml of assay media. The assay is then conducted as described above.--

The paragraph, beginning at page 488, line 15, has been amended as follows:

--Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50:50 without glycine, 1% glutamine, 10mM Hepes, 10% FBS, 10 ng/ml bFGF), were plated on 96-well microtiter ViewPlates-96 (Packard Instrument Company Part #6005182) microtiter plates at a cell density of  $2 \times 10^4$  cells/well. The day after plating, the cells were washed three times with buffer (HBSS plus 10 mM Hepes), leaving 100  $\mu$ l/well. Then 100  $\mu$ l/well of 8  $\mu$ M Fluo-3 (2x) was added. The cells were incubated for 1.5 hours at 37°C/5% CO<sub>2</sub>. After incubation, the cells were then washed 3x with buffer (described above) leaving 100  $\mu$ l/well. Test samples of the PRO polypeptides were prepared on different 96-well plates at 5x concentration in buffer. The positive control corresponded to 50  $\mu$ M ionomycin (5x); the negative control corresponded to Protein 32. Cell plate and sample plates were run on a FLIPR® (fluorometric imaging microplate reader) (Molecular Devices) machine. The FLIPR® (fluorometric imaging microplate reader) machine added 25  $\mu$ l of test sample to the cells, and readings were taken every second for one minute, then every 3 seconds for the next three minutes.--

The paragraph, beginning at page 490, line 28, has been amended as follows:

--The starting material for the screen was genomic DNA isolated from a variety of cancers. The DNA is quantitated precisely, e.g., fluorometrically. As a negative control, DNA was isolated from the cells of ten normal healthy individuals which was pooled and used as assay

controls for the gene copy in healthy individuals (not shown). The 5' nuclease assay (for example, ~~TaqMan~~<sup>TM</sup> TAQMAN®) and real-time quantitative PCR (for example, ~~ABI Prism~~ PRISM® 7700 Sequence Detection System<sup>TM</sup> (Perkin Elmer, Applied Biosystems Division, Foster City, CA)), were used to find genes potentially amplified in certain cancers. The results were used to determine whether the DNA encoding PRO1295, PRO1293, PRO1265, PRO1303, PRO1269, PRO1410, PRO1317, PRO1780, PRO1555, PRO1755, PRO1558, PRO1759 and PRO1788 is over-represented in any of the primary lung or colon cancers or cancer cell lines or breast cancer cell lines that were screened. The primary lung cancers were obtained from individuals with tumors of the type and stage as indicated in Table 7. An explanation of the abbreviations used for the designation of the primary tumors listed in Table 7 and the primary tumors and cell lines referred to throughout this example has been given hereinbefore.--

The paragraph, beginning at page 491, line 1, has been amended as follows:

--The results of the ~~TaqMan~~ TAQMAN® (polymerase chain reaction (PCR) test) are reported in delta ( $\Delta$ ) Ct units. One unit corresponds to 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold, 3 units to 8-fold amplification and so on. Quantitation was obtained using primers and a ~~TaqMan~~ TAQMAN® fluorescent probe derived from the PRO1295-, PRO1293-, PRO1265-, PRO1303-, PRO1269-, PRO1410-, PRO1317-, PRO1780-, PRO1555-, PRO1755-, PRO1558-, PRO1759- and PRO1788-encoding gene. Regions of PRO1295, PRO1293, PRO1265, PRO1303, PRO1269, PRO1410, PRO1317, PRO1780, PRO1555, PRO1755, PRO1558, PRO1759 and PRO1788 which are most likely to contain unique nucleic acid sequences and which are least likely to have spliced out introns are preferred for the primer and probe derivation, e.g., 3'-untranslated regions. The sequences for the primers and probes (forward, reverse and probe) used for the PRO1295, PRO1293, PRO1265, PRO1303, PRO1269, PRO1410, PRO1317, PRO1780, PRO1555, PRO1755, PRO1558, PRO1759 and PRO1788 gene amplification analysis were as follows:--

The paragraph, beginning at page 494, line 2, has been amended as follows:

--The 5' nuclease procedure is run on a real-time quantitative PCR device such as the ~~ABI Prism~~ PRISM® 7700<sup>TM</sup> Sequence Detection System. The system consists of a thermocycler,

laser, charge-coupled device (CCD) camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.--

The paragraph, beginning at page 497, line 25, has been amended as follows:

--The fluorometrically determined concentration was then used to dilute each sample to 10 ng/ $\mu$ l in ddH<sub>2</sub>O. This was done simultaneously on all template samples for a single ~~TaqMan~~ TAQMAN® plate assay, and with enough material to run 500-1000 assays. The samples were tested in triplicate with ~~TaqMan~~ TAQMAN® primers and probe both B-actin and GAPDH on a single plate with normal human DNA and no-template controls. The diluted samples were used provided that the CT value of normal human DNA subtracted from test DNA was +/- 1 Ct. The diluted, lot-qualified genomic DNA was stored in 1.0 ml aliquots at -80°C. Aliquots which were subsequently to be used in the gene amplification assay were stored at 4°C. Each 1 ml aliquot is enough for 8-9 plates or 64 tests.--

The paragraph, beginning at page 505, line 12, has been amended as follows:

--In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over ~~Lympholyte M~~ LYMPHOLYTE®-M (cell separation medium) (Organon Teknika) centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to  $1 \times 10^7$  cells/ml of assay media. The assay is then conducted as described above.--

The paragraph, beginning at page 505, line 23, has been amended as follows:

--This assay shows that certain polypeptides of the invention act to induce proliferation of mammalian kidney mesangial cells and, therefore, are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies

associated with Schönlein-Henoch purpura, celiac disease, dermatitis herpetiformis or Crohn disease. The assay is performed as follows. On day one, mouse kidney mesangial cells are plated on a 96 well plate in growth media (3:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 medium, 95% fetal bovine serum, 5% supplemented with 14 mM HEPES) and grown overnight. On day 2, PRO polypeptides are diluted at 2 concentrations(1% and 0.1%) in serum-free medium and added to the cells. Control samples are serum-free medium alone. On day 4, 20 $\mu$ l of the Cell Titer 96 Aqueous one solution reagent (Progenia) was added to each well and the ~~colorimetric~~ colorimetric reaction was allowed to proceed for 2 hours. The absorbance (OD) is then measured at 490 nm. A positive in the assay is anything that gives an absorbance reading which is at least 15% above the control reading.--

**Amendment to the Drawing:**

In FIGURE 74, under the section titled "Transmembrane domains:", the amino acid residue numbers "217-287" have been amended to recite "271-287".